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Revised 04/24/2003

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/442,489D*

DATE: 09/30/2003
TIME: 16:00:35

INPUT SET: S37023.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: ALBERTSEN, HANS
ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
VOGELSTEIN, BERT
--> **WHITE, RAYMOND L.**

(ii) TITLE OF INVENTION: APC ANTIBODIES

(iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Allegretti, LTD
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001-4598

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/442,489
(B) FILING DATE: 18-NOV-1999
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/452,654
(B) FILING DATE: 25-MAY-1995

```
46       (vi) PRIOR APPLICATION DATA:
47             (A) APPLICATION NUMBER: US 08/289,548
48             (B) FILING DATE: 12-AUG-1994
49
50       (vi) PRIOR APPLICATION DATA:
51             (A) APPLICATION NUMBER: US 07/741,940
52             (B) FILING DATE: 08-AUG-1001
53
54
55    (viii) ATTORNEY/AGENT INFORMATION:
56             (A) NAME: Kagan, Sarah A.
57             (B) REGISTRATION NUMBER: 32,141
58             (C) REFERENCE/DOCKET NUMBER: 1107.035574
59
60       (ix) TELECOMMUNICATION INFORMATION:
61             (A) TELEPHONE: 202-508-9100
62             (B) TELEFAX: 202-508-9299
63
64
```

ERRORED SEQUENCES FOLLOW:

```
1761  (2) INFORMATION FOR SEQ ID NO:7:
1762
1763       (i) SEQUENCE CHARACTERISTICS:
--> 1764        (A) LENGTH: 2843 amino acids
1765            (B) TYPE: amino acid
1766            (C) STRANDEDNESS: single
1767            (D) TOPOLOGY: linear
1768
1769      (ii) MOLECULE TYPE: protein
1770
1771     (vi) ORIGINAL SOURCE:
1772           (A) ORGANISM: Homo sapiens
1773
1774    (vii) IMMEDIATE SOURCE:
1775           (B) CLONE: APC
1776
1777
1778
1779     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
1780
1781      Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
1782      1               5                   10                  15
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1784      Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
1785                  20                  25                  30
1786
1787      His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
1788            35                  40                  45
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2842 amino-acids

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1789
1790        Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
1791            50                  55                  60
1792
1793        Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
1794        65                  70                  75                  80
1795
1796        Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
1797                        85                  90                  95
1798
1799        Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
1800                    100                 105                 110
1801
1802        Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
1803                115                 120                 125
1804
1805        Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
1806            130                 135                 140
1807
1808        Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
1809        145                 150                 155                 160
1810
1811        Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Thr Glu Asn
1812                        165                 170                 175
1813
1814    Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala
1815                180                 185                 190
1816
1817    Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp
1818            195                 200                 205
1819
1820    Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu
1821        210                 215                 220
1822
1823    Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu
1824    225                 230                 235                 240
1825
1826    Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala
1827                    245                 250                 255
1828
1829    Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr
1830                260                 265                 270
1831
1832    Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala
1833            275                 280                 285
1834
1835    Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr
1836        290                 295                 300
1837
1838    Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met
1839    305                 310                 315                 320
1840
1841    Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met
```

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                  325                 330                 335

Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu
            340                 345                 350

Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu
        355                 360                 365

Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala
    370                 375                 380

Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly Arg
385                 390                 395                 400

Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr Cys
                405                 410                 415

Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp Gln
            420                 425                 430

Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro Ala
        435                 440                 445

Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His Ala
    450                 455                 460

Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln Val
465                 470                 475                 480

Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr Leu
                485                 490                 495

Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp Val
            500                 505                 510

Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala Leu
        515                 520                 525

Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile Ala
    530                 535                 540

Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys Lys
545                 550                 555                 560

Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala Leu
                565                 570                 575

Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu Trp
            580                 585                 590

Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala Val
        595                 600                 605
```

```
1895  Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln
1896       610                 615                 620
1897
1898  Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn
1899  625                 630                 635                 640
1900
1901  Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu Arg
1902                  645                 650                 655
1903
1904  Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser
1905              660                 665                 670
1906
1907  Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala
1908          675                 680                 685
1909
1910  Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser
1911       690                 695                 700
1912
1913  Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly
1914  705                 710                 715                 720
1915
1916  Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr
1917                  725                 730                 735
1918
1919  Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His
1920              740                 745                 750
1921
1922  Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu
1923          755                 760                 765
1924
1925  Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His
1926       770                 775                 780
1927
1928  Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe
1929  785                 790                 795                 800
1930
1931  Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly
1932                  805                 810                 815
1933
1934  Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser
1935              820                 825                 830
1936
1937  Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp
1938          835                 840                 845
1939
1940  Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro
1941       850                 855                 860
1942
1943  Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser
1944  865                 870                 875                 880
1945
1946  Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile
1947                  885                 890                 895
```

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1948
1949  His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His
1950              900                 905                 910
1951
1952  Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His
1953          915                 920                 925
1954
1955  Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg
1956      930                 935                 940
1957
1958  Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn
1959  945                 950                 955                 960
1960
1961  Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg Gly
1962                  965                 970                 975
1963
1964  Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys
1965              980                 985                 990
1966
1967  Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His
1968          995                 1000                1005
1969
1970  Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile
1971      1010                1015                1020
1972
1973  Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln
1974  1025                1030                1035                1040
1975
1976  Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile Glu
1977                  1045                1050                1055
1978
1979  Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr
1980              1060                1065                1070
1981
1982  Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys Phe
1983          1075                1080                1085
1984
1985  Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg
1986      1090                1095                1100
1987
1988  Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly Ile
1989  1105                1110                1115                1120
1990
1991  Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp
1992                  1125                1130                1135
1993
1994  Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln His
1995              1140                1145                1150
1996
1997  Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu
1998          1155                1160                1165
1999
2000  Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr
```

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2001      1170                1175                1180
2002
2003  Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser
2004  1185                1190                1195                1200
2005
2006  Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu Asn
2007                  1205                1210                1215
2008
2009  Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro
2010              1220                1225                1230
2011
2012  Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys
2013          1235                1240                1245
2014
2015  Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu
2016      1250                1255                1260
2017
2018  Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser
2019  1265                1270                1275                1280
2020
2021  Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp
2022                  1285                1290                1295
2023
2024  Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr
2025              1300                1305                1310
2026
2027  Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His
2028          1315                1320                1325
2029
2030  Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu
2031      1330                1335                1340
2032
2033  Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro
2034  1345                1350                1355                1360
2035
2036  Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val
2037                  1365                1370                1375
2038
2039  Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu
2040              1380                1385                1390
2041
2042  Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro
2043          1395                1400                1405
2044
2045  Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp
2046      1410                1415                1420
2047
2048  Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro
2049  1425                1430                1435                1440
2050
2051  Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala
2052                  1445                1450                1455
2053
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2054  Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn
2055              1460                1465                1470
2056
2057  Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu
2058          1475                1480                1485
2059
2060  His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser
2061      1490                1495                1500
2062
2063  Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu
2064  1505                1510                1515                1520
2065
2066  Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr
2067                  1525                1530                1535
2068
2069  Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala
2070              1540                1545                1550
2071
2072  Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp
2073          1555                1560                1565
2074  Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr
2075      1570                1575                1580
2076
2077  Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu
2078  1585                1590                1595                1600
2079
2080  Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu
2081                  1605                1610                1615
2082
2083  Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr
2084              1620                1625                1630
2085
2086  Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile
2087          1635                1640                1645
2088
2089  Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro
2090      1650                1655                1660
2091
2092  Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln Ser
2093  1665                1670                1675                1680
2094
2095  Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr
2096                  1685                1690                1695
2097
2098  Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu
2099              1700                1705                1710
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2101  Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn
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2104  Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys
2105      1730                1735                1740
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2107  Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn
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2110  Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val Lys
2111                  1765                1770                1775
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2113  Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala
2114              1780                1785                1790
2115
2116  Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys
2117          1795                1800                1805
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2119  Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp
2120      1810                1815                1820
2121
2122  Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp
2123  1825                1830                1835                1840
2124
2125  Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser
2126                  1845                1850                1855
2127
2128  Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Asp Val Asp
2129              1860                1865                1870
2130
2131  Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu
2132          1875                1880                1885
2133
2134  Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln Gln
2135      1890                1895                1900
2136
2137  Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly
2138  1905                1910                1915                1920
2139
2140
2141  Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser
2142                  1925                1930                1935
2143
2144  Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn
2145              1940                1945                1950
2146
2147  Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu
2148          1955                1960                1965
2149
2150  Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu
2151      1970                1975                1980
2152
2153  Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys
2154  1985                1990                1995                2000
2155
2156  Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr
2157                  2005                2010                2015
2158
2159  Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp
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2160              2020                2025                2030
2161
2162  Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys
2163          2035                2040                2045
2164
2165  Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro
2166      2050                2055                2060
2167
2168  Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys
2169  2065                2070                2075                2080
2170
2171  Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu
2172                  2085                2090                2095
2173
2174  Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser
2175              2100                2105                2110
2176
2177  Ser Leu His Gln Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser
2178          2115                2120                2125
2179
2180  Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly
2181      2130                2135                2140
2182
2183  Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser
2184  2145                2150                2155                2160
2185
2186  Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu
2187                  2165                2170                2175
2188
2189  Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys
2190              2180                2185                2190
2191
2192  Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile
2193          2195                2200                2205
2194
2195  Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser
2196      2210                2215                2220
2197
2198  Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser
2199  2225                2230                2235                2240
2200
2201  Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala
2202                  2245                2250                2255
2203
2204  Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly
2205              2260                2265                2270
2206
2207
2208  Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr
2209          2275                2280                2285
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2211  Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg
2212      2290                2295                2300
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2213
2214  Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile
2215  2305                2310                2315                2320
2216
2217  Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser
2218                  2325                2330                2335
2219
2220  Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr
2221              2340                2345                2350
2222
2223  Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro
2224          2355                2360                2365
2225
2226  Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser
2227      2370                2375                2380
2228
2229  Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu
2230  2385                2390                2395                2400
2231
2232  Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser
2233                  2405                2410                2415
2234
2235  Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu
2236              2420                2425                2430
2237
2238  Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser
2239          2435                2440                2445
2240
2241  Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu
2242      2450                2455                2460
2243
2244  Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr
2245  2465                2470                2475                2480
2246
2247  Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser
2248                  2485                2490                2495
2249
2250  Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro
2251              2500                2505                2510
2252
2253  Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala
2254          2515                2520                2525
2255
2256  Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly
2257      2530                2535                2540
2258
2259  Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val
2260  2545                2550                2555                2560
2261
2262  Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser
2263                  2565                2570                2575
2264
2265  Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn
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2266                2580                    2585                    2590
2267
2268   Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys
2269           2595                    2600                    2605
2270
2271   Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser
2272       2610                    2615                    2620
2273
2274
2275   Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys
2276   2625                    2630                    2635                    2640
2277
2278   Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val
2279                   2645                    2650                    2655
2280
2281   Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg
2282               2660                    2665                    2670
2283
2284   Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys
2285           2675                    2680                    2685
2286
2287   Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn
2288       2690                    2695                    2700
2289
2290   Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg
2291   2705                    2710                    2715                    2720
2292
2293   Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu
2294                   2725                    2730                    2735
2295
2296   Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu
2297               2740                    2745                    2750
2298
2299   Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser Lys
2300           2755                    2760                    2765
2301
2302   His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn
2303       2770                    2775                    2780
2304
2305   Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg
2306   2785                    2790                    2795                    2800
2307
2308   Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp
2309                   2805                    2810                    2815
2310
2311   Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg
2312               2820                    2825                    2830
2313
2314   His Ser Gly Ser Tyr Leu Val Thr Ser Val
2315           2835                    2840
2316                                                    +
2317                                                    total 2842 not 2843

3913   (2) INFORMATION FOR SEQ ID NO:95:
```

```
     3914
     3915   (i) SEQUENCE CHARACTERISTICS:
--> 3916   (A) LENGTH: 24 base pairs
     3917   (B) TYPE: nucleic acid
     3918   (C) STRANDEDNESS: single
     3919   (D) TOPOLOGY: linear
     3920
     3921   (ii) MOLECULE TYPE: cDNA
     3922
     3923   (vi) ORIGINAL SOURCE:
     3924   (A) ORGANISM: Homo sapiens
     3925
     3926   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:
     3927
--> 3928   AGAAGGATCCCTTGTGCAGTGTGGA24
     3929
```

25

25 → All non-coding nucleotides need to be grouped in 10's (tens) with a space between each group.

```
     3930   (2) INFORMATION FOR SEQ ID NO:96:
     3931
     3932   (i) SEQUENCE CHARACTERISTICS:
     3933   (A) LENGTH: 24 base pairs
     3934   (B) TYPE: nucleic acid
     3935   (C) STRANDEDNESS: single
     3936   (D) TOPOLOGY: linear
     3937
     3938   (ii) MOLECULE TYPE: cDNA
     3939
     3940   (vi) ORIGINAL SOURCE:
--> 3941   (A) Homo sapiens
     3942
     3943   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:
     3944
     3945   GACAGGATCCTGAAGCTGAGTTTG24
     3946
```

(A) Organism: Homo sapiens. Mandatory heading missing throughout sequences.

→ Same error throughout

```
     3947   (2) INFORMATION FOR SEQ ID NO:97:
     3948
     3949   (i) SEQUENCE CHARACTERISTICS:
     3950   (A) LENGTH: 18 base pairs
     3951   (B) TYPE: nucleic acid
     3952   (C) STRANDEDNESS: single
     3953   (D) TOPOLOGY: linear
     3954
     3955   (ii) MOLECULE TYPE: cDNA
     3956
     3957   (vi) ORIGINAL SOURCE:
--> 3958   (A) Homo sapiens
     3959
     3960   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:
     3961
     3962   TCAGAAAGTGCTGAAGAG18
     3963
```

```
     3964   (2) INFORMATION FOR SEQ ID NO:98:
```

```
      3965
      3966   (i) SEQUENCE CHARACTERISTICS:
      3967   (A) LENGTH: 19 base pairs
      3968   (B) TYPE: nucleic acid
      3969   (C) STRANDEDNESS: single
      3970   (D) TOPOLOGY: linear
      3971
      3972   (ii) MOLECULE TYPE: cDNA
      3973
      3974   (vi) ORIGINAL SOURCE:
-->   3975   (A) Homo sapiens
      3976
      3977   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:
      3978
      3979   GGAATAATTAGGTCTCCAA19          same
      3980
-------------------------------------------------------------------------------
      3981   (2) INFORMATION FOR SEQ ID NO:99:
      3982
      3983   (i) SEQUENCE CHARACTERISTICS:
      3984   (A) LENGTH: 21 base pairs
      3985   (B) TYPE: nucleic acid
      3986   (C) STRANDEDNESS: single
      3987   (D) TOPOLOGY: linear
      3988
      3989   (ii) MOLECULE TYPE: cDNA
      3990
      3991   (vi) ORIGINAL SOURCE:
-->   3992   (A) Homo sapiens
      3993
      3994   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
      3995
      3996   GCAAATCCTAAGAGAGAACAA21        same
      3997
-------------------------------------------------------------------------------
      3998   (2) INFORMATION FOR SEQ ID NO:100:
      3999
      4000   (i) SEQUENCE CHARACTERISTICS:
      4001   (A) LENGTH: 19 base pairs
      4002   (B) TYPE: nucleic acid
      4003   (C) STRANDEDNESS: single
      4004   (D) TOPOLOGY: linear
      4005
      4006   (ii) MOLECULE TYPE: cDNA
      4007
      4008   (vi) ORIGINAL SOURCE:
-->   4009   (A) Homo sapiens
      4010
      4011   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
      4012
      4013   GATGGCAAGCTTGAGCCAG19          same
      4014
-------------------------------------------------------------------------------
      4015   (2) INFORMATION FOR SEQ ID NO:101:
```

4016
4017 (i) SEQUENCE CHARACTERISTICS:
4018 (A) LENGTH: 18 base pairs
4019 (B) TYPE: nucleic acid
4020 (C) STRANDEDNESS: single
4021 (D) TOPOLOGY: linear
4022
4023 (ii) MOLECULE TYPE: cDNA
4024
4025 (vi) ORIGINAL SOURCE:
--> 4026 (A) Homo sapiens
4027
4028 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
4029
4030 GTTCCAGCAGTGTCACAG18 same
4031

4032 (2) INFORMATION FOR SEQ ID NO:102:
4033
4034 (i) SEQUENCE CHARACTERISTICS:
4035 (A) LENGTH: 18 base pairs
4036 (B) TYPE: nucleic acid
4037 (C) STRANDEDNESS: single
4038 (D) TOPOLOGY: linear
4039
4040 (ii) MOLECULE TYPE: cDNA
4041
4042 (vi) ORIGINAL SOURCE:
--> 4043 (A) Homo sapiens
4044
4045 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
4046
--> 4047 GGGAGATTTCGCTCCTGA02 18 group in 10's
4048
4049

4050 (2) INFORMATION FOR SEQ ID NO:103:
4051
4052 (i) SEQUENCE CHARACTERISTICS:
4053 (A) LENGTH: 23 base pairs
4054 (B) TYPE: nucleic acid
4055 (C) STRANDEDNESS: single
4056 (D) TOPOLOGY: linear
4057
4058 (ii) MOLECULE TYPE: cDNA
4059
4060 (vi) ORIGINAL SOURCE:
--> 4061 (A) Homo sapiens
4062
4063 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
4064
4065 AGTACAAGGA TGCCAATATT ATG 23
4066

```
     4067   (2) INFORMATION FOR SEQ ID NO:104:
     4068
     4069   (i) SEQUENCE CHARACTERISTICS:
     4070   (A) LENGTH: 23 base pairs
     4071   (B) TYPE: nucleic acid
     4072   (C) STRANDEDNESS: single
     4073   (D) TOPOLOGY: linear
     4074
     4075   (ii) MOLECULE TYPE: cDNA
     4076
     4077   (vi) ORIGINAL SOURCE:
-->  4078   (A) Homo sapiens
     4079
     4080   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
     4081
     4082   ACTTCTATCT TTTTCAGAAC GAG                                    23
     4083
```

```
     4084   (2) INFORMATION FOR SEQ ID NO:105:
     4085
     4086   (i) SEQUENCE CHARACTERISTICS:
     4087   (A) LENGTH: 23 base pairs
     4088   (B) TYPE: nucleic acid
     4089   (C) STRANDEDNESS: single
     4090   (D) TOPOLOGY: linear
     4091
     4092   (ii) MOLECULE TYPE: cDNA
     4093
     4094   (vi) ORIGINAL SOURCE:
-->  4095   (A) Homo sapiens
     4096
     4097   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:
     4098
     4099   ATTTGAATAC TACAGTGTTA CCC                                    23
     4100
```

```
     4101   (2) INFORMATION FOR SEQ ID NO:106:
     4102
     4103   (i) SEQUENCE CHARACTERISTICS:
     4104   (A) LENGTH: 24 base pairs
     4105   (B) TYPE: nucleic acid
     4106   (C) STRANDEDNESS: single
     4107   (D) TOPOLOGY: linear
     4108
     4109   (ii) MOLECULE TYPE: cDNA
     4110
     4111   (vi) ORIGINAL SOURCE:
-->  4112   (A) Homo sapiens
     4113
     4114   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:
     4115
     4116   CTTGTATTCT AATTTGGCAT AAGG                                    24
```

4117

4118 (2) INFORMATION FOR SEQ ID NO:107:
4119
4120 (i) SEQUENCE CHARACTERISTICS:
4121 (A) LENGTH: 22 base pairs
4122 (B) TYPE: nucleic acid
4123 (C) STRANDEDNESS: single
4124 (D) TOPOLOGY: linear
4125
4126 (ii) MOLECULE TYPE: cDNA
4127
4128 (vi) ORIGINAL SOURCE:
--> 4129 (A) Homo sapiens
4130
4131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
4132
4133 CTGCCCATAC ACATTCAAAC AC 22
4134

4135 (2) INFORMATION FOR SEQ ID NO:108:
4136
4137 (i) SEQUENCE CHARACTERISTICS:
4138 (A) LENGTH: 21 base pairs
4139 (B) TYPE: nucleic acid
4140 (C) STRANDEDNESS: single
4141 (D) TOPOLOGY: linear
4142
4143 (ii) MOLECULE TYPE: cDNA
4144
4145 (vi) ORIGINAL SOURCE:
--> 4146 (A) Homo sapiens
4147
4148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:
4149
4150 TGTTTGCGTC TTGCCCATCT T 21
4151

4152 (2) INFORMATION FOR SEQ ID NO:109:
4153
4154 (i) SEQUENCE CHARACTERISTICS:
4155 (A) LENGTH: 24 base pairs
4156 (B) TYPE: nucleic acid
4157 (C) STRANDEDNESS: single
4158 (D) TOPOLOGY: linear
4159
4160 (ii) MOLECULE TYPE: cDNA
4161
4162 (vi) ORIGINAL SOURCE:
--> 4163 (A) Homo sapiens
4164
4165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
4166

```
     4167  AGTCTTAAAT ATTCAGATGA GCAG                                    24
     4168
```

```
     4169  (2) INFORMATION FOR SEQ ID NO:110:
     4170
     4171  (i) SEQUENCE CHARACTERISTICS:
     4172  (A) LENGTH: 26 base pairs
     4173  (B) TYPE: nucleic acid
     4174  (C) STRANDEDNESS: single
     4175  (D) TOPOLOGY: linear
     4176
     4177  (ii) MOLECULE TYPE: cDNA
     4178
     4179  (vi) ORIGINAL SOURCE:
-->  4180  (A) Homo sapiens
     4181
     4182  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
     4183
     4184  GTTTCTCTTC ATTATATTTT ATGCTA                                  26
     4185
```

```
     4186  (2) INFORMATION FOR SEQ ID NO:111:
     4187
     4188  (i) SEQUENCE CHARACTERISTICS:
     4189  (A) LENGTH: 23 base pairs
     4190  (B) TYPE: nucleic acid
     4191  (C) STRANDEDNESS: single
     4192  (D) TOPOLOGY: linear
     4193
     4194  (ii) MOLECULE TYPE: cDNA
     4195
     4196  (vi) ORIGINAL SOURCE:
-->  4197  (A) Homo sapiens
     4198
     4199  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
     4200
     4201  AAGCCTACCA ATTATAGTGA ACG                                     23
     4202
```

```
     4203  (2) INFORMATION FOR SEQ ID NO:112:
     4204
     4205  (i) SEQUENCE CHARACTERISTICS:
     4206  (A) LENGTH: 23 base pairs
     4207  (B) TYPE: nucleic acid
     4208  (C) STRANDEDNESS: single
     4209  (D) TOPOLOGY: linear
     4210
     4211  (ii) MOLECULE TYPE: cDNA
     4212
     4213  (vi) ORIGINAL SOURCE:
-->  4214  (A) Homo sapiens
     4215
     4216  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:
```

4217
4218 AGCTGATGAC AAAGATGATA ATC 23
4219

4220 (2) INFORMATION FOR SEQ ID NO:113:
4221
4222 (i) SEQUENCE CHARACTERISTICS:
4223 (A) LENGTH: 24 base pairs
4224 (B) TYPE: nucleic acid
4225 (C) STRANDEDNESS: single
4226 (D) TOPOLOGY: linear
4227
4228 (ii) MOLECULE TYPE: cDNA
4229
4230 (vi) ORIGINAL SOURCE:
--> 4231 **(A) Homo sapiens**
4232
4233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
4234
4235 AAGAAACAAT ACAGACTTAT TGTG 24
4236

4237 (2) INFORMATION FOR SEQ ID NO:114:
4238
4239 (i) SEQUENCE CHARACTERISTICS:
4240 (A) LENGTH: 20 base pairs
4241 (B) TYPE: nucleic acid
4242 (C) STRANDEDNESS: single
4243 (D) TOPOLOGY: linear
4244
4245 (ii) MOLECULE TYPE: cDNA
4246
4247 (vi) ORIGINAL SOURCE:
--> 4248 **(A) Homo sapiens**
4249
4250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:
4251
4252 ATGAGTGGGG TCTCCTGAAC 20
4253

4254 (2) INFORMATION FOR SEQ ID NO:115:
4255
4256 (i) SEQUENCE CHARACTERISTICS:
4257 (A) LENGTH: 21 base pairs
4258 (B) TYPE: nucleic acid
4259 (C) STRANDEDNESS: single
4260 (D) TOPOLOGY: linear
4261
4262 (ii) MOLECULE TYPE: cDNA
4263
4264 (vi) ORIGINAL SOURCE:
--> 4265 **(A) Homo sapiens**
4266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATCTCCCTCC AAAAGTGGTG C 21

---

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TCCATCTGGA GTACTTTCTG TG 22

---

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGTAAATGCT GCAGTTCAGA GG 22

---

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

4317
4318 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
4319
4320 CCGTGGCATA TCATCCCCC 19
4321

4322 (2) INFORMATION FOR SEQ ID NO:119:
4323
4324 (i) SEQUENCE CHARACTERISTICS:
4325 (A) LENGTH: 22 base pairs
4326 (B) TYPE: nucleic acid
4327 (C) STRANDEDNESS: single
4328 (D) TOPOLOGY: linear
4329
4330 (ii) MOLECULE TYPE: cDNA
4331
4332 (vi) ORIGINAL SOURCE:
--> 4333 **(A) Homo sapiens**
4334
4335 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
4336 CCCAGACTGC TTCAAAATTA CC 22
4337

4338 (2) INFORMATION FOR SEQ ID NO:120:
4339
4340 (i) SEQUENCE CHARACTERISTICS:
4341 (A) LENGTH: 21 base pairs
4342 (B) TYPE: nucleic acid
4343 (C) STRANDEDNESS: single
4344 (D) TOPOLOGY: linear
4345
4346 (ii) MOLECULE TYPE: cDNA
4347
4348 (vi) ORIGINAL SOURCE:
--> 4349 **(A) Homo sapiens**
4350
4351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
4352
4353 GAGCCTCATC TGTACTTCTG C 21
4354

4355 (2) INFORMATION FOR SEQ ID NO:121:
4356
4357 (i) SEQUENCE CHARACTERISTICS:
4358 (A) LENGTH: 21 base pairs
4359 (B) TYPE: nucleic acid
4360 (C) STRANDEDNESS: single
4361 (D) TOPOLOGY: linear
4362
4363 (ii) MOLECULE TYPE: cDNA
4364
4365 (vi) ORIGINAL SOURCE:
--> 4366 **(A) Homo sapiens**

4367
4368 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
4369
4370 CCCTCCAAAT GAGTTAGCTG C 21
4371

4372 (2) INFORMATION FOR SEQ ID NO:122:
4373
4374 (i) SEQUENCE CHARACTERISTICS:
4375 (A) LENGTH: 23 base pairs
4376 (B) TYPE: nucleic acid
4377 (C) STRANDEDNESS: single
4378 (D) TOPOLOGY: linear
4379
4380 (ii) MOLECULE TYPE: cDNA
4381
4382 (vi) ORIGINAL SOURCE:
--> 4383 **(A) Homo sapiens**
4384
4385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:
4386
4387 TTGTGGTATA GGTTTTACTG GTG 23
4388

4389 (2) INFORMATION FOR SEQ ID NO:123:
4390
4391 (i) SEQUENCE CHARACTERISTICS:
4392 (A) LENGTH: 23 base pairs
4393 (B) TYPE: nucleic acid
4394 (C) STRANDEDNESS: single
4395 (D) TOPOLOGY: linear
4396
4397 (ii) MOLECULE TYPE: cDNA
4398
4399 (vi) ORIGINAL SOURCE:
--> 4400 **(A) Homo sapiens**
4401
4402 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:
4403
4404 ACCCAACAAA AATCAGTTAG ATG 23
4405

4406 (2) INFORMATION FOR SEQ ID NO:124:
4407
4408 (i) SEQUENCE CHARACTERISTICS:
4409 (A) LENGTH: 21 base pairs
4410 (B) TYPE: nucleic acid
4411 (C) STRANDEDNESS: single
4412 (D) TOPOLOGY: linear
4413
4414 (ii) MOLECULE TYPE: cDNA
4415
4416 (vi) ORIGINAL SOURCE:

--> 4417 (A) Homo sapiens
4418
4419 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:
4420
4421 GTGGCTGGTA ACTTTAGCCT C 21
4422

4423 (2) INFORMATION FOR SEQ ID NO:125:
4424
4425 (i) SEQUENCE CHARACTERISTICS:
4426 (A) LENGTH: 21 base pairs
4427 (B) TYPE: nucleic acid
4428 (C) STRANDEDNESS: single
4429 (D) TOPOLOGY: linear
4430
4431 (ii) MOLECULE TYPE: cDNA
4432
4433 (vi) ORIGINAL SOURCE:
--> 4434 (A) Homo sapiens
4435
4436 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:
4437
4438 ATGATGTTGA CCTTTCCAGG G 21
4439

4440 (2) INFORMATION FOR SEQ ID NO:126:
4441
4442 (i) SEQUENCE CHARACTERISTICS:
4443 (A) LENGTH: 24 base pairs
4444 (B) TYPE: nucleic acid
4445 (C) STRANDEDNESS: single
4446 (D) TOPOLOGY: linear
4447
4448 (ii) MOLECULE TYPE: cDNA
4449
4450 (vi) ORIGINAL SOURCE:
--> 4451 (A) Homo sapiens
4452
4453 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:
4454
4455 ATTGTGTAAC TTTTCATCAG TTGC 24
4456

4457 (2) INFORMATION FOR SEQ ID NO:127:
4458
4459 (i) SEQUENCE CHARACTERISTICS:
4460 (A) LENGTH: 21 base pairs
4461 (B) TYPE: nucleic acid
4462 (C) STRANDEDNESS: single
4463 (D) TOPOLOGY: linear
4464
4465 (ii) MOLECULE TYPE: cDNA
4466

4467 (vi) ORIGINAL SOURCE:
--> 4468 (A) Homo sapiens
4469
4470 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:
4471
4472 AAAGACATAC CAGACAGAGG G 21
4473

4474 (2) INFORMATION FOR SEQ ID NO:128:
4475
4476 (i) SEQUENCE CHARACTERISTICS:
4477 (A) LENGTH: 21 base pairs
4478 (B) TYPE: nucleic acid
4479 (C) STRANDEDNESS: single
4480 (D) TOPOLOGY: linear
4481
4482 (ii) MOLECULE TYPE: cDNA
4483
4484 (vi) ORIGINAL SOURCE:
--> 4485 (A) Homo sapiens
4486
4487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
4488
4489 CTTTTTTGGC ATTGCGGAGC T 21
4490

4491 (2) INFORMATION FOR SEQ ID NO:129:
4492
4493 (i) SEQUENCE CHARACTERISTICS:
4494 (A) LENGTH: 22 base pairs
4495 (B) TYPE: nucleic acid
4496 (C) STRANDEDNESS: single
4497 (D) TOPOLOGY: linear
4498
4499 (ii) MOLECULE TYPE: cDNA
4500
4501 (vi) ORIGINAL SOURCE:
--> 4502 (A) Homo sapiens
4503
4504 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:
4505
4506 AAGATGACCT GTTGCAGGAA TG 22
4507

4508 (2) INFORMATION FOR SEQ ID NO:130:
4509
4510 (i) SEQUENCE CHARACTERISTICS:
4511 (A) LENGTH: 24 base pairs
4512 (B) TYPE: nucleic acid
4513 (C) STRANDEDNESS: single
4514 (D) TOPOLOGY: linear
4515
4516 (ii) MOLECULE TYPE: cDNA

```
     4517
     4518  (vi) ORIGINAL SOURCE:
-->  4519  (A) Homo sapiens
     4520
     4521  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:
     4522
     4523  GAATCAGACC AAGCTTGTCT AGAT                                        24
     4524
```

```
     4525  (2) INFORMATION FOR SEQ ID NO:131:
     4526
     4527  (i) SEQUENCE CHARACTERISTICS:
     4528  (A) LENGTH: 24 base pairs
     4529  (B) TYPE: nucleic acid
     4530  (C) STRANDEDNESS: single
     4531  (D) TOPOLOGY: linear
     4532
     4533  (ii) MOLECULE TYPE: cDNA
     4534
     4535  (vi) ORIGINAL SOURCE:
-->  4536  (A) Homo sapiens
     4537
     4538  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:
     4539
     4540  CAATAGTAAG TAGTTTACAT CAAG                                        24
     4541
```

```
     4542  (2) INFORMATION FOR SEQ ID NO:132:
     4543
     4544  (i) SEQUENCE CHARACTERISTICS:
     4545  (A) LENGTH: 22 base pairs
     4546  (B) TYPE: nucleic acid
     4547  (C) STRANDEDNESS: single
     4548  (D) TOPOLOGY: linear
     4549
     4550  (ii) MOLECULE TYPE: cDNA
     4551
     4552  (vi) ORIGINAL SOURCE:
-->  4553  (A) Homo sapiens
     4554
     4555  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:
     4556
     4557  AAACAGGACT TGTACTGTAG GA                                          22
     4558
```

```
     4559  (2) INFORMATION FOR SEQ ID NO:133:
     4560
     4561  (i) SEQUENCE CHARACTERISTICS:
     4562  (A) LENGTH: 21 base pairs
     4563  (B) TYPE: nucleic acid
     4564  (C) STRANDEDNESS: single
     4565  (D) TOPOLOGY: linear
     4566
```

```
     4567   (ii) MOLECULE TYPE: cDNA
     4568
     4569   (vi) ORIGINAL SOURCE:
-->  4570   (A) Homo sapiens
     4571
     4572   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:
     4573
     4574   CAGCCCCTTC AAGCAAACAT C                                          21
     4575
```

```
     4576   (2) INFORMATION FOR SEQ ID NO:134:
     4577
     4578   (i) SEQUENCE CHARACTERISTICS:
     4579   (A) LENGTH: 22 base pairs
     4580   (B) TYPE: nucleic acid
     4581   (C) STRANDEDNESS: single
     4582   (D) TOPOLOGY: linear
     4583
     4584   (ii) MOLECULE TYPE: cDNA
     4585
     4586   (vi) ORIGINAL SOURCE:
-->  4587   (A) Homo sapiens
     4588
     4589   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:
     4590
     4591   GAGGACTTAT TCCATTTCTA CC                                         22
     4592
```

```
     4593   (2) INFORMATION FOR SEQ ID NO:135:
     4594
     4595   (i) SEQUENCE CHARACTERISTICS:
     4596   (A) LENGTH: 20 base pairs
     4597   (B) TYPE: nucleic acid
     4598   (C) STRANDEDNESS: single
     4599   (D) TOPOLOGY: linear
     4600
     4601   (ii) MOLECULE TYPE: cDNA
     4602
     4603   (vi) ORIGINAL SOURCE:
-->  4604   (A) Homo sapiens
     4605
     4606   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:
     4607
     4608   CAGTCTCCTG GCCGAAACTC                                            20
     4609
```

```
     4610   (2) INFORMATION FOR SEQ ID NO:136:
     4611
     4612   (i) SEQUENCE CHARACTERISTICS:
     4613   (A) LENGTH: 22 base pairs
     4614   (B) TYPE: nucleic acid
     4615   (C) STRANDEDNESS: single
     4616   (D) TOPOLOGY: linear
```

```
     4617
     4618   (ii) MOLECULE TYPE: cDNA
     4619
     4620   (vi) ORIGINAL SOURCE:
-->  4621   (A) Homo sapiens
     4622
     4623   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:
     4624
     4625   GTTGACTGGC GTACTAATAC AG                                        22
     4626
```

```
     4627   (2) INFORMATION FOR SEQ ID NO:137:
     4628
     4629   (i) SEQUENCE CHARACTERISTICS:
     4630   (A) LENGTH: 23 base pairs
     4631   (B) TYPE: nucleic acid
     4632   (C) STRANDEDNESS: single
     4633   (D) TOPOLOGY: linear
     4634
     4635   (ii) MOLECULE TYPE: cDNA
     4636
     4637   (vi) ORIGINAL SOURCE:
-->  4638   (A) Homo sapiens
     4639
     4640   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:
     4641
     4642   TGGTAATGGA GCCAATAAAA AGG                                       23
     4643
```

```
     4644   (2) INFORMATION FOR SEQ ID NO:138:
     4645
     4646   (i) SEQUENCE CHARACTERISTICS:
     4647   (A) LENGTH: 20 base pairs
     4648   (B) TYPE: nucleic acid
     4649   (C) STRANDEDNESS: single
     4650   (D) TOPOLOGY: linear
     4651
     4652   (ii) MOLECULE TYPE: cDNA
     4653
     4654   (vi) ORIGINAL SOURCE:
-->  4655   (A) Homo sapiens
     4656
     4657   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:
     4658
     4659   TGGGACTTTT CGCCATCCAC                                           20
     4660
```

```
     4661   (2) INFORMATION FOR SEQ ID NO:139:
     4662
     4663   (i) SEQUENCE CHARACTERISTICS:
     4664   (A) LENGTH: 22 base pairs
     4665   (B) TYPE: nucleic acid
     4666   (C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TGTCTCTATC CACACATTCG TC 22

---

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ATGTTTTTCA TCCTCACTTT TTGC 24

---

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGAGAAGAAC TGGAAGTTCA TC 22

---

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid

```
     4717   (C) STRANDEDNESS: single
     4718   (D) TOPOLOGY: linear
     4719
     4720   (ii) MOLECULE TYPE: cDNA
     4721
     4722   (vi) ORIGINAL SOURCE:
-->  4723   (A) Homo sapiens
     4724
     4725   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:
     4726
     4727   TTGAATCTTT AATGTTTGGA TTTGC                                    25
     4728
```

```
     4729   (2) INFORMATION FOR SEQ ID NO:143:
     4730
     4731   (i) SEQUENCE CHARACTERISTICS:
     4732   (A) LENGTH: 21 base pairs
     4733   (B) TYPE: nucleic acid
     4734   (C) STRANDEDNESS: single
     4735   (D) TOPOLOGY: linear
     4736
     4737   (ii) MOLECULE TYPE: cDNA
     4738
     4739   (vi) ORIGINAL SOURCE:
-->  4740   (A) Homo sapiens
     4741
     4742   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:
     4743
     4744   TCTCCCACAG GTAATACTCC C                                        21
     4745
```

```
     4746   (2) INFORMATION FOR SEQ ID NO:144:
     4747
     4748   (i) SEQUENCE CHARACTERISTICS:
     4749   (A) LENGTH: 21 base pairs
     4750   (B) TYPE: nucleic acid
     4751   (C) STRANDEDNESS: single
     4752   (D) TOPOLOGY: linear
     4753
     4754   (ii) MOLECULE TYPE: cDNA
     4755
     4756   (vi) ORIGINAL SOURCE:
-->  4757   (A) Homo sapiens
     4758
     4759   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:
     4760
     4761   GCTACAACTG AATGGGGTAC G                                        21
     4762
```

```
     4763   (2) INFORMATION FOR SEQ ID NO:145:
     4764
     4765   (i) SEQUENCE CHARACTERISTICS:
     4766   (A) LENGTH: 22 base pairs
```

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAGGACAAAA TAATCCTGTC CC 22

---

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
--> **(A) Homo sapiens**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ATTTTCTTAC TTTCATTCTT CCTC 24

---

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) Topology: mandatory heading missing throughout amino acid sequences
(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
--> **(A) Artificial sequence (consensus)**

--> **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:**

Phe Xaa Val Glu Xaa Thr Pro Xaa Cys Phe Ser Arg Xaa Ser Ser Leu Ser Ser Leu
1 5 10 15

Ser
20

---

(2) INFORMATION FOR SEQ ID NO:148:

```
     4818
     4819   (i) SEQUENCE CHARACTERISTICS:
     4820   (A) LENGTH: 20 amino acids
     4821   (B) TYPE: amino acid
     4822   (D) same
     4823   (ii) MOLECULE TYPE: protein
     4824
     4825   (vi) ORIGINAL SOURCE:
-->  4826   (A) Homo sapiens
     4827
-->  4828   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:
     4829
     4830   Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu
     4831    1               5                  10                  15
     4832   Ser Ser Leu Ser
     4833                20
     4834
```

```
     4835   (2) INFORMATION FOR SEQ ID NO:149:
     4836
     4837   (i) SEQUENCE CHARACTERISTICS:
     4838   (A) LENGTH: 20 amino acids
     4839   (B) TYPE: amino acid
     4840   (D)
     4841   (ii) MOLECULE TYPE: protein
     4842
     4843   (vi) ORIGINAL SOURCE:
-->  4844   (A) Homo sapiens
     4845
-->  4846   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:
     4847
     4848   His Thr Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val
     4849    1               5                  10                  15
     4850   Ser Ser Leu Asp
     4851                20
     4852
```

```
     4853   (2) INFORMATION FOR SEQ ID NO:150:
     4854
     4855   (i) SEQUENCE CHARACTERISTICS:
     4856   (A) LENGTH: 20 amino acids
     4857   (B) TYPE: amino acid
     4858   (D)
     4859   (ii) MOLECULE TYPE: protein
     4860
     4861   (vi) ORIGINAL SOURCE:
-->  4862   (A) Homo sapiens
     4863
-->  4864   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
     4865
     4866   Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser Leu
     4867    1               5                  10                  15
     4868   Ser Ala Leu Ser
```

```
     4869                20
     4870
--------------------------------------------------------------------------------
     4871   (2) INFORMATION FOR SEQ ID NO:151:
     4872
     4873   (i) SEQUENCE CHARACTERISTICS:
     4874   (A) LENGTH: 20 amino acids
     4875   (B) TYPE: amino acid
     4876   (D)
     4877   (ii) MOLECULE TYPE: protein
     4878
     4879   (vi) ORIGINAL SOURCE:
-->  4880   (A) Homo sapiens
     4881
-->  4882   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:
     4883
     4884   Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr Ser Leu
     4885    1               5                  10                  15
     4886   Ser Asp Leu Thr
     4887                20
     4888
--------------------------------------------------------------------------------
     4889   (2) INFORMATION FOR SEQ ID NO:152:
     4890
     4891   (i) SEQUENCE CHARACTERISTICS:
     4892   (A) LENGTH: 20 amino acids
     4893   (B) TYPE: amino acid
     4894   (D)
     4895   (ii) MOLECULE TYPE: protein
     4896
     4897   (vi) ORIGINAL SOURCE:
-->  4898   (A) Homo sapiens
     4899
-->  4900   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:
     4901
     4902   Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu
     4903    1               5                  10                  15
     4904   Ser Ser Leu Asp
     4905                20
     4906
--------------------------------------------------------------------------------
     4907   (2) INFORMATION FOR SEQ ID NO:153:
     4908
     4909   (i) SEQUENCE CHARACTERISTICS:
     4910   (A) LENGTH: 20 amino acids
     4911   (B) TYPE: amino acid
     4912   (D)
     4913   (ii) MOLECULE TYPE: protein
     4914
     4915   (vi) ORIGINAL SOURCE:
-->  4916   (A) Homo sapiens
     4917
-->  4918   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:
```

```
4919
4920   Phe Ala Ile Glu Asn Thr Pro Val Cys Pro Ser His Asn Ser Ser Leu
4921    1               5                  10                  15
4922   Ser Ser Leu Ser
4923                20
4924
```

```
4925   (2) INFORMATION FOR SEQ ID NO:154:
4926
4927   (i) SEQUENCE CHARACTERISTICS:
4928   (A) LENGTH: 20 amino acids
4929   (B) TYPE: amino acid
4930   (D)
4931   (ii) MOLECULE TYPE: protein
4932
4933   (vi) ORIGINAL SOURCE:
--> 4934   (A) Homo sapiens
4935
--> 4936   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:
4937
4938   Arg His Val Glu Asp Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu
4939    1               5                  10                  15
4940   Ser Ser Leu Ser
4941                20
4942
--> 4943   ??
4944
4945
4946
4947
4948
4949
4950
4951
4952
4953
4954
```
